

**Does Not Comply
Corrected Diskette Needed**



OIIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/043,774A

DATE: 04/25/2002

TIME: 14:31:09

Input Set : N:\Crif3\04102002\J043774.raw

Output Set: N:\CRF3\04252002\J043774A.raw

1 <110> APPLICANT: University of Illinois at
2 <120> TITLE OF INVENTION: HUMAN HEMATOPOIETIC
3 <130> FILE REFERENCE: MBHB: CU08/PPA<160> 17 <170> PatentIn

*Sample page
if for matting
error. Please
Contact:
Robert Wax at:
703-306-4119 or
703-308-4214*

ERRORED SEQUENCES

5 <210> SEQ ID NO: 1<211> 2328<212> DNA<213> Homo sapiens<220><221> CDS<222>

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E--> 7 <212> TYPE:

W--> 8 <213> ORGANISM:

9 <223> OTHER INFORMATION: Human Hiwi Protein

W--> 0 <160> NUMBER OF SEQ ID NOS:

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14	tca aaa aca ggt tct tca ggc att ata gta agg tta agc act aac cat	96
15	Ser Lys Thr Gly Ser Ser Gly Ile Ile Val Arg Leu Ser Thr Asn His	
16	20 25 30	
17	ttc cgg ctg aca tcc cgt ccc cag tgg gcc tta tat cag tat cac att	144
18	Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala Leu Tyr Gln Tyr His Ile	
19	35 40 45	
20	gac tat aac cca ctg atg gaa gcc aga aga ctc cgt tca gct ctt ctt	192
21	Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg Leu Arg Ser Ala Leu Leu	
22	50 55 60	
23	ttt caa cac gaa gat cta att gga aag tgt cat gct ttt gat gga acg	240
24	Phe Gln His Glu Asp Leu Ile Gly Lys Cys His Ala Phe Asp Gly Thr	
25	65 70 75 80	
26	ata tta ttt tta cct aaa aga cta cag caa aag gtt act gaa gtt ttt	288
27	Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln Lys Val Thr Glu Val Phe	
28	85 90 95	
29	agt aag acc cgg aat gga gag gat gtg agg ata acg atc act tta aca	336
30	Ser Lys Thr Arg Asn Gly Glu Asp Val Arg Ile Thr Ile Thr Leu Thr	
31	100 105 110	
32	aat gaa ctt cca cct aca tca cca act tgt ttg cag ttc tat aat att	384
33	Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys Leu Gln Phe Tyr Asn Ile	
34	115 120 125	
35	att ttc agg agg ctt ttg aaa atc atg aat ttg caa caa att gga cga	432
36	Ile Phe Arg Arg Leu Leu Lys Ile Met Asn Leu Gln Gln Ile Gly Arg	
37	130 135 140	
38	aat tat tat aac cca aat gac cca att gat att cca agt cac agg ttg	480
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43		165	170	175	
44	atc atg ctc tgc act gac gtt agc cat aaa gtc ctt cga agt gag act				576
45	Ile Met Leu Cys Thr Asp Val Ser His Lys Val Leu Arg Ser Glu Thr				
46		180	185	190	
47	gtt ttg gat ttc atg ttc aac ttt tat cat cag aca gaa gaa cat aaa				624
48	Val Leu Asp Phe Met Phe Asn Phe Tyr His Gln Thr Glu Glu His Lys				
49		195	200	205	
50	ttt caa gaa caa gtt tcc aaa gaa cta ata ggt tta gtt gtt ctt acc				672
51	Phe Gln Glu Gln Val Ser Lys Glu Leu Ile Gly Leu Val Val Leu Thr				
52		210	215	220	
53	aag tat aac aat aag aca tac aga gtg gat gat att gac tgg gac cag				720
54	Lys Tyr Asn Asn Lys Thr Tyr Arg Val Asp Asp Ile Asp Trp Asp Gln				
55		225	230	235	240
56	aat ccc aag agc acc ttt aag aaa gcc gac ggc tct gaa gtc agc ttc				768
57	Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp Gly Ser Glu Val Ser Phe				
58		245	250	255	
59	tta gaa tac tac agg aag caa tac aac caa gag atc acc gac ttg aag				816
60	Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln Glu Ile Thr Asp Leu Lys				
61		260	265	270	
62	cag cct gtc ttg gtc agc cag ccc aag aga agg cgg ggc cct ggg ggg				864
63	Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Arg Gly Pro Gly Gly				
64		275	280	285	
65	aca ctg cca ggg cct gcc atg ctc att cct gag ctc tgc tat ctt aca				912
66	Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu Cys Tyr Leu Thr				
67		290	295	300	
68	ggt cta act gat aaa atg cgt aat gat ttt aac gtg atg aaa gac tta				960
69	Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val Met Lys Asp Leu				
70		305	310	315	320
71	gcc gtt cat aca aga cta act cca gag caa agg cag cgt gaa gtg gga				1008
72	Ala Val His Thr Arg Leu Thr Pro Glu Gln Arg Gln Arg Glu Val Gly				
73		325	330	335	
74	cga ctc att gat tac att cat aaa aac gat aat gtt caa agg gag ctt				1056
75	Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val Gln Arg Glu Leu				
76		340	345	350	
77	cga gac tgg ggt ttg agc ttt gat tcc aac tta ctg tcc ttc tca gga				1104
78	Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn Leu Leu Ser Phe Ser Gly				
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80	aga att ttg caa aca gaa aag att cac caa ggt gga aaa aca ttt gat				1152
81	Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Gly Lys Thr Phe Asp				
82		370	375	380	
83	tac aat cca caa ttt gca gat tgg tcc aaa gaa aca aga ggt gca cca				1200
84	Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys Glu Thr Arg Gly Ala Pro				
85		385	390	395	400
86	tta att agt gtt aag cca cta gat aac tgg ctg ttg atc tat acg cga				1248
87	Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg				
88		405	410	415	

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89	aga aat tat gaa gca gcc aat tca ttg ata caa aat cta ttt aaa gtt	1296
90	Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn Leu Phe Lys Val	
91	420 425 430	
92	aca cca gcc atg ggc atg caa atg aga aaa gca ata atg att gaa gtg	1344
93	Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile Met Ile Glu Val	
94	435 440 445	
95	gat gac aga act gaa gcc tac tta aga gtc tta cag caa aag gtc aca	1392
96	Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln Gln Lys Val Thr	
97	450 455 460	
98	gca gac acc cag ata gtt gtc tgt ctg ttg tca agt aat cgg aag gac	1440
99	Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser Asn Arg Lys Asp	
100	465 470 475 480	
101	aaa tac gat gct att aaa aaa tac ctg tgt aca gat tgc cct acc cca	1488
102	Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro	
103	485 490 495	
104	agt cag tgt gtg gtg gcc cga acc tta ggc aaa cag caa act gtc atg	1536
105	Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln Gln Thr Val Met	
106	500 505 510	
107	gcc att gct aca aag att gcc cta cag atg aac tgc aag atg gga gga	1584
108	Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys Lys Met Gly Gly	
109	515 520 525	
110	gag ctc tgg agg gtg gac atc ccc ctg aag ctc gtg atg atc gtt ggc	1632
111	Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val Met Ile Val Gly	
112	530 535 540	
113	atc gat tgt tac cat gac atg aca gct ggg cgg agg tca atc gca gga	1680
114	Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Arg Ser Ile Ala Gly	
115	545 550 555 560	
116	ttt gtt gcc agc atc aat gaa ggg atg acc cgc tgg ttc tca cgc tgc	1728
117	Phe Val Ala Ser Ile Asn Glu Gly Met Thr Arg Trp Phe Ser Arg Cys	
118	565 570 575	
119	ata ttt cag gat aga gga cag gag ctg gta gat ggg ctc aaa gtc tgc	1776
120	Ile Phe Gln Asp Arg Gly Gln Glu Leu Val Asp Gly Leu Lys Val Cys	
121	580 585 590	
122	ctg caa gcg gct ctg agg gct tgg aat agc tgc aat gag tac atg ccc	1824
123	Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys Asn Glu Tyr Met Pro	
124	595 600 605	
125	agc cgg atc atc gtg tac cgc gat ggc gta gga gac ggc cag ctg aaa	1872
126	Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp Gly Gln Leu Lys	
127	610 615 620	
128	aca ctg gtg aac tac gaa gtg cca cag ttt ttg gat tgt cta aaa tcc	1920
129	Thr Leu Val Asn Tyr Glu Val Pro Gln Phe Leu Asp Cys Leu Lys Ser	
130	625 630 635 640	
131	att ggt aga ggt tac aac cct aga cta acg gta att gtg gtg aag aaa	1968
132	Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr Val Ile Val Val Lys Lys	
133	645 650 655	
134	aga gtg aac acc aga ttt ttt gct cag tct gga gga aga ctt cag aat	2016
135	Arg Val Asn Thr Arg Phe Phe Ala Gln Ser Gly Gly Arg Leu Gln Asn	
136	660 665 670	
137	cca ctt cct gga aca gtt att gat gta gag gtt acc aga cca gaa tgg	2064

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140      tat gac ttt ttt atc gtg agc cag gct gtg aga agt ggt agt gtt tct      2112
141      Tyr Asp Phe Phe Ile Val Ser Gln Ala Val Arg Ser Gly Ser Val Ser
142              690              695              700
143      ccc aca cat tac aat gtc atc tat gac aac agc ggc ctg aag cca gac      2160
144      Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly Leu Lys Pro Asp
145      705              710              715              720
146      cac ata cag cgc ttg acc tac aag ctg tgc cac atc tat tac aac tgg      2208
147      His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile Tyr Tyr Asn Trp
148              725              730              735
149      cca ggt gtc att cgt gtt cct gct cct tgc cag tac gcc cac aag ctg      2256
150      Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr Ala His Lys Leu
151              740              745              750
152      gct ttt ctt gtt ggc cag agt att cac aga gag cca aat ctg tca ctg      2304
153      Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro Asn Leu Ser Leu
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155      tca aac cgc ctt tac tac ctc taa      2328
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167      20              25              30
168      Phe Arg Leu Thr Ser Arg Pro Gln Trp Ala Leu Tyr Gln Tyr His Ile
169      35              40              45
170      Asp Tyr Asn Pro Leu Met Glu Ala Arg Arg Leu Arg Ser Ala Leu Leu
171      50              55              60
172      Phe Gln His Glu Asp Leu Ile Gly Lys Cys His Ala Phe Asp Gly Thr
173      65              70              75              80
174      Ile Leu Phe Leu Pro Lys Arg Leu Gln Gln Lys Val Thr Glu Val Phe
175      85              90              95
176      Ser Lys Thr Arg Asn Gly Glu Asp Val Arg Ile Thr Ile Thr Leu Thr
177      100             105             110
178      Asn Glu Leu Pro Pro Thr Ser Pro Thr Cys Leu Gln Phe Tyr Asn Ile
179      115             120             125
180      Ile Phe Arg Arg Leu Leu Lys Ile Met Asn Leu Gln Ile Gly Arg
181      130             135             140
182      Asn Tyr Tyr Asn Pro Asn Asp Pro Ile Asp Ile Pro Ser His Arg Leu
183      145             150             155             160
184      Val Ile Trp Pro Gly Phe Thr Thr Ser Ile Leu Gln Tyr Glu Asn Ser
185      165             170             175
186      Ile Met Leu Cys Thr Asp Val Ser His Lys Val Leu Arg Ser Glu Thr
187      180             185             190

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188 Val Leu Asp Phe Met Phe Asn Phe Tyr His Gln Thr Glu Glu His Lys
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190 Phe Gln Glu Gln Val Ser Lys Glu Leu Ile Gly Leu Val Val Leu Thr
191           210           215           220
192 Lys Tyr Asn Asn Lys Thr Tyr Arg Val Asp Asp Ile Asp Trp Asp Gln
193           225           230           235           240
194 Asn Pro Lys Ser Thr Phe Lys Lys Ala Asp Gly Ser Glu Val Ser Phe
195           245           250           255
196 Leu Glu Tyr Tyr Arg Lys Gln Tyr Asn Gln Glu Ile Thr Asp Leu Lys
197           260           265           270
198 Gln Pro Val Leu Val Ser Gln Pro Lys Arg Arg Arg Gly Pro Gly Gly
199           275           280           285
200 Thr Leu Pro Gly Pro Ala Met Leu Ile Pro Glu Leu Cys Tyr Leu Thr
201           290           295           300
202 Gly Leu Thr Asp Lys Met Arg Asn Asp Phe Asn Val Met Lys Asp Leu
203           305           310           315           320
204 Ala Val His Thr Arg Leu Thr Pro Glu Gln Arg Gln Arg Glu Val Gly
205           325           330           335
206 Arg Leu Ile Asp Tyr Ile His Lys Asn Asp Asn Val Gln Arg Glu Leu
207           340           345           350
208 Arg Asp Trp Gly Leu Ser Phe Asp Ser Asn Leu Leu Ser Phe Ser Gly
209           355           360           365
210 Arg Ile Leu Gln Thr Glu Lys Ile His Gln Gly Gly Lys Thr Phe Asp
211           370           375           380
212 Tyr Asn Pro Gln Phe Ala Asp Trp Ser Lys Glu Thr Arg Gly Ala Pro
213           385           390           395           400
214 Leu Ile Ser Val Lys Pro Leu Asp Asn Trp Leu Leu Ile Tyr Thr Arg
215           405           410           415
216 Arg Asn Tyr Glu Ala Ala Asn Ser Leu Ile Gln Asn Leu Phe Lys Val
217           420           425           430
218 Thr Pro Ala Met Gly Met Gln Met Arg Lys Ala Ile Met Ile Glu Val
219           435           440           445
220 Asp Asp Arg Thr Glu Ala Tyr Leu Arg Val Leu Gln Gln Lys Val Thr
221           450           455           460
222 Ala Asp Thr Gln Ile Val Val Cys Leu Leu Ser Ser Asn Arg Lys Asp
223           465           470           475           480
224 Lys Tyr Asp Ala Ile Lys Lys Tyr Leu Cys Thr Asp Cys Pro Thr Pro
225           485           490           495
226 Ser Gln Cys Val Val Ala Arg Thr Leu Gly Lys Gln Gln Thr Val Met
227           500           505           510
228 Ala Ile Ala Thr Lys Ile Ala Leu Gln Met Asn Cys Lys Met Gly Gly
229           515           520           525
230 Glu Leu Trp Arg Val Asp Ile Pro Leu Lys Leu Val Met Ile Val Gly
231           530           535           540
232 Ile Asp Cys Tyr His Asp Met Thr Ala Gly Arg Arg Ser Ile Ala Gly
233           545           550           555           560
234 Phe Val Ala Ser Ile Asn Glu Gly Met Thr Arg Trp Phe Ser Arg Cys
235           565           570           575
236 Ile Phe Gln Asp Arg Gly Gln Glu Leu Val Asp Gly Leu Lys Val Cys

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237          580          585          590
238  Leu Gln Ala Ala Leu Arg Ala Trp Asn Ser Cys Asn Glu Tyr Met Pro
239          595          600          605
240  Ser Arg Ile Ile Val Tyr Arg Asp Gly Val Gly Asp Gly Gln Leu Lys
241          610          615          620
242  Thr Leu Val Asn Tyr Glu Val Pro Gln Phe Leu Asp Cys Leu Lys Ser
243          625          630          635          640
244  Ile Gly Arg Gly Tyr Asn Pro Arg Leu Thr Val Ile Val Val Lys Lys
245          645          650          655
246  Arg Val Asn Thr Arg Phe Phe Ala Gln Ser Gly Gly Arg Leu Gln Asn
247          660          665          670
248  Pro Leu Pro Gly Thr Val Ile Asp Val Glu Val Thr Arg Pro Glu Trp
249          675          680          685
250  Tyr Asp Phe Phe Ile Val Ser Gln Ala Val Arg Ser Gly Ser Val Ser
251          690          695          700
252  Pro Thr His Tyr Asn Val Ile Tyr Asp Asn Ser Gly Leu Lys Pro Asp
253          705          710          715          720
254  His Ile Gln Arg Leu Thr Tyr Lys Leu Cys His Ile Tyr Tyr Asn Trp
255          725          730          735
256  Pro Gly Val Ile Arg Val Pro Ala Pro Cys Gln Tyr Ala His Lys Leu
257          740          745          750
258  Ala Phe Leu Val Gly Gln Ser Ile His Arg Glu Pro Asn Leu Ser Leu
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Ready
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347 <223> OTHER INFORMATION: PIWI protein

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353 Phe Arg Gly Ser Ser Ser Gly Asp Pro Arg Ala Asp Pro Arg Ile Glu
354 35 40 45
355 Ala Ser Arg Glu Arg Arg Ala Leu Glu Glu Ala Pro Arg Arg Glu Gly
356 50 55 60
357 Gly Pro Pro Glu Arg Lys Pro Trp Gly Asp Gln Tyr Asp Tyr Leu Asn
358 65 70 75 80
359 Thr Arg Pro Val Glu Leu Val Ser Lys Lys Gly Thr Asp Gly Val Pro
360 85 90 95
361 Val Met Leu Gln Thr Asn Phe Phe Arg Leu Lys Thr Lys Pro Glu Trp
362 100 105 110
363 Arg Ile Val His Tyr His Val Glu Phe Glu Pro Ser Ile Glu Asn Pro
364 115 120 125
365 Arg Val Arg Met Gly Val Leu Ser Asn His Ala Asn Leu Leu Gly Ser
366 130 135 140
367 Gly Tyr Leu Phe Asp Gly Leu Gln Leu Phe Thr Thr Arg Lys Phe Glu
368 145 150 155 160
369 Gln Glu Ile Thr Val Leu Ser Gly Lys Ser Lys Leu Asp Ile Glu Tyr
370 165 170 175
371 Lys Ile Ser Ile Lys Phe Val Gly Phe Ile Ser Cys Ala Glu Pro Arg
372 180 185 190
373 Phe Leu Gln Val Leu Asn Leu Ile Leu Arg Arg Ser Met Lys Gly Leu
374 195 200 205
375 Asn Leu Glu Leu Val Gly Arg Asn Leu Phe Asp Pro Arg Ala Lys Ile
376 210 215 220
377 Glu Ile Arg Glu Phe Lys Met Glu Leu Trp Pro Gly Tyr Glu Thr Ser
378 225 230 235 240
379 Ile Arg Gln His Glu Lys Asp Ile Leu Leu Gly Thr Glu Ile Thr His
380 245 250 255
381 Lys Val Met Arg Thr Glu Thr Ile Tyr Asp Ile Met Arg Arg Cys Ser
382 260 265 270
383 His Asn Pro Ala Arg His Gln Asp Glu Val Arg Val Asn Val Leu Asp
384 275 280 285
385 Leu Ile Val Leu Thr Asp Tyr Asn Asn Arg Thr Tyr Arg Ile Asn Asp
386 290 295 300
387 Val Asp Phe Gly Gln Thr Pro Lys Ser Thr Phe Ser Cys Lys Gly Arg
388 305 310 315 320
389 Asp Ile Ser Phe Val Glu Tyr Tyr Leu Thr Lys Tyr Asn Ile Arg Ile
390 325 330 335
391 Arg Asp His Asn Gln Pro Leu Leu Ile Ser Lys Asn Arg Asp Lys Ala
392 340 345 350
393 Leu Lys Thr Asn Ala Ser Glu Leu Val Val Leu Ile Pro Glu Leu Cys
394 355 360 365

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TIME: 14:31:10

Input Set : N:\Crf3\04102002\J043774.raw

Output Set: N:\CRF3\04252002\J043774A.raw

```

395 Arg Val Thr Gly Leu Asn Ala Glu Met Arg Ser Asn Phe Gln Leu Met
396      370      375      380
397 Arg Ala Met Ser Ser Tyr Thr Arg Met Asn Pro Lys Gln Arg Thr Asp
398      385      390      395      400
399 Arg Leu Arg Ala Phe Asn His Arg Leu Gln Asn Thr Pro Glu Ser Val
400      405      410      415
401 Lys Val Leu Arg Asp Trp Asn Met Glu Leu Asp Lys Asn Val Thr Glu
402      420      425      430
403 Val Gln Gly Arg Ile Ile Gly Gln Gln Asn Ile Val Phe His Asn Gly
404      435      440      445
405 Lys Val Pro Ala Gly Glu Asn Ala Asp Trp Gln Arg His Phe Arg Asp
406      450      455      460
407 Gln Arg Met Leu Thr Thr Pro Ser Asp Gly Leu Asp Arg Trp Ala Val
408      465      470      475      480
409 Ile Ala Pro Gln Arg Asn Ser His Glu Leu Arg Thr Leu Leu Asp Ser
410      485      490      495
411 Leu Tyr Arg Ala Ala Ser Gly Met Gly Leu Arg Ile Arg Ser Pro Gln
412      500      505      510
413 Glu Phe Ile Ile Tyr Asp Asp Arg Thr Gly Thr Tyr Val Arg Ala Met
414      515      520      525
415 Asp Asp Cys Val Arg Ser Asp Pro Lys Leu Ile Leu Cys Leu Val Pro
416      530      535      540
417 Asn Asp Asn Ala Glu Arg Tyr Ser Ser Ile Lys Lys Arg Gly Tyr Val
418      545      550      555      560
419 Asp Arg Ala Val Pro Thr Gln Val Val Thr Leu Lys Thr Thr Lys Lys
420      565      570      575
421 Pro Tyr Ser Leu Met Ser Ile Ala Thr Lys Ile Ala Ile Gln Leu Asn
422      580      585      590
423 Cys Lys Leu Gly Tyr Thr Pro Trp Met Ile Glu Leu Pro Leu Ser Gly
424      595      600      605
425 Leu Met Thr Ile Gly Phe Asp Ile Ala Lys Ser Thr Arg Asp Arg Lys
426      610      615      620
427 Arg Ala Tyr Gly Ala Leu Ile Ala Ser Met Asp Leu Gln Gln Asn Ser
428      625      630      635      640
429 Thr Tyr Phe Ser Thr Val Thr Glu Cys Ser Ala Phe Asp Val Leu Ala
430      645      650      655
431 Asn Thr Leu Trp Pro Met Ile Ala Lys Ala Leu Arg Gln Tyr Gln His
432      660      665      670
433 Glu His Arg Lys Leu Pro Ser Arg Ile Val Phe Tyr Arg Asp Gly Val
434      675      680      685
435 Ser Ser Gly Ser Leu Lys Gln Leu Phe Glu Phe Glu Val Lys Asp Ile
436      690      695      700
437 Ile Glu Lys Leu Lys Thr Glu Tyr Ala Arg Val Gln Leu Ser Pro Pro
438      705      710      715      720
439 Gln Leu Ala Tyr Ile Val Val Thr Arg Ser Met Asn Thr Arg Phe Phe
440      725      730      735
441 Leu Asn Gly Gln Asn Pro Pro Pro Gly Thr Ile Val Asp Asp Val Ile
442      740      745      750
443 Thr Leu Pro Glu Arg Tyr Asp Phe Tyr Leu Val Ser Gln Gln Val Arg

```

RAW SEQUENCE LISTING

DATE: 04/25/2002

PATENT APPLICATION: US/10/043,774A

TIME: 14:31:10

Input Set : N:\Crf3\04102002\J043774.raw

Output Set: N:\CRF3\04252002\J043774A.raw

```

444          755          760          765
445      Gln Gly Thr Val Ser Pro Thr Ser Tyr Asn Val Leu Tyr Ser Ser Met
446          770          775          780
447      Gly Leu Ser Pro Glu Lys Met Gln Lys Leu Thr Tyr Lys Met Cys His
448      785          790          795          800
449      Leu Tyr Tyr Asn Trp Ser Gly Thr Thr Arg Val Pro Ala Val Cys Gln
450          805          810          815
451      Tyr Ala Lys Lys Leu Ala Thr Leu Val Gly Thr Asn Leu His Ser Ile
452          820          825          830
453      Pro Gln Asn Ala Leu Glu Lys Lys Phe Tyr Tyr Leu
454          835          840
456 <210> SEQ ID NO: 14<211> 29<212> DNA<213> Artificial Sequence<220><223> CD34
W--> 457 hematopoietic cell cDNA forward primer
E--> 458 <211> LENGTH:
E--> 459 <212> TYPE:
W--> 460 <213> ORGANISM:
461 <400> SEQUENCE: 14
462      atgatctttg gtgtgaacac aaggcagaa 29
464 <210> SEQ ID NO: 15<211> 31<212> DNA<213> Artificial Sequence<220><223> CD34
W--> 465 hematopoietic cell cDNA reverse primer
E--> 466 <211> LENGTH:
E--> 467 <212> TYPE:
W--> 468 <213> ORGANISM:
469 <400> SEQUENCE: 15
470      gaggtagtaa aggcggtttg acagtgcag a 31
472 <210> SEQ ID NO: 16<211> 24<212> DNA<213> Artificial Sequence<220><223> human hiwi
W--> 473 gene forward primer
E--> 474 <211> LENGTH:
E--> 475 <212> TYPE:
W--> 476 <213> ORGANISM:
477 <400> SEQUENCE: 16
478      ccttgccagt acgcccacaa gctg 24
480 <210> SEQ ID NO: 17<211> 27<212> DNA<213> Artificial Sequence<220><223> human hiwi
W--> 481 gene reverse primer
E--> 482 <211> LENGTH:
E--> 483 <212> TYPE:
W--> 484 <213> ORGANISM:
485 <400> SEQUENCE: 17
486      cccacctat ggttgtagtg agcatcc 27

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 04/25/2002
PATENT APPLICATION: US/10/043,774A TIME: 14:31:11

Input Set : N:\Crf3\04102002\J043774.raw
Output Set: N:\CRF3\04252002\J043774A.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 263
Seq#:3; Line(s) 271
Seq#:6; Line(s) 295
Seq#:7; Line(s) 303
Seq#:8; Line(s) 311
Seq#:9; Line(s) 319
Seq#:10; Line(s) 327
Seq#:11; Line(s) 335
Seq#:15; Line(s) 472
Seq#:16; Line(s) 480

VERIFICATION SUMMARY

DATE: 04/25/2002

PATENT APPLICATION: US/10/043,774A

TIME: 14:31:11

Input Set : N:\Crf3\04102002\J043774.raw

Output Set: N:\CRF3\04252002\J043774A.raw

L:6 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:7 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:8 M:201 W: Mandatory field data missing, <213> ORGANISM
L:0 M:282 W: Numeric Field Identifier Missing, <160> is required.
L:10 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:1
L:160 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:161 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:162 M:201 W: Mandatory field data missing, <213> ORGANISM
L:163 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:2 differs:1
L:264 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:265 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:266 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:267 M:201 W: Mandatory field data missing, <213> ORGANISM
L:272 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:273 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:274 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:275 M:201 W: Mandatory field data missing, <213> ORGANISM
L:280 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:281 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:282 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:283 M:201 W: Mandatory field data missing, <213> ORGANISM
L:288 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:289 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:290 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:291 M:201 W: Mandatory field data missing, <213> ORGANISM
L:296 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:297 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:298 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:299 M:201 W: Mandatory field data missing, <213> ORGANISM
L:304 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:305 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:306 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:307 M:201 W: Mandatory field data missing, <213> ORGANISM
L:312 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:313 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:314 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:315 M:201 W: Mandatory field data missing, <213> ORGANISM
L:320 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:321 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:322 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:323 M:201 W: Mandatory field data missing, <213> ORGANISM
L:328 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:329 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:330 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:331 M:201 W: Mandatory field data missing, <213> ORGANISM
L:336 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:337 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:338 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:

VERIFICATION SUMMARY

DATE: 04/25/2002

PATENT APPLICATION: US/10/043,774A

TIME: 14:31:11

Input Set : N:\Crf3\04102002\J043774.raw

Output Set: N:\CRF3\04252002\J043774A.raw

L:339 M:201 W: Mandatory field data missing, <213> ORGANISM
L:344 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:345 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:346 M:201 W: Mandatory field data missing, <213> ORGANISM
L:348 M:200 E: Mandatory Header Field missing, <220> not found for SEQ ID#:13
L:457 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:458 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:459 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:460 M:201 W: Mandatory field data missing, <213> ORGANISM
L:465 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:466 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:467 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:468 M:201 W: Mandatory field data missing, <213> ORGANISM
L:473 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:474 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:475 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:476 M:201 W: Mandatory field data missing, <213> ORGANISM
L:481 M:259 W: Allowed number of lines exceeded, <210> SEQ ID NO
L:482 M:210 E: (40) Invalid Number of Sequences, LENGTH:
L:483 M:310 E: (3) Wrong or Missing Sequence Type, TYPE:
L:484 M:201 W: Mandatory field data missing, <213> ORGANISM
L:0 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (0) Counted (17)

STATISTICS SUMMARY

DATE: 04/25/2002

PATENT APPLICATION: US/10/043,774A - TIME: 14:31:11

Input Set : N:\Crf3\04102002\J043774.raw

Output Set: N:\CRF3\04252002\J043774A.raw

Application Serial Number: US/10/043,774A

Alpha or Numeric: Numeric

Application Class:

Application File Date: 03-29-2002

Art Unit: OIPE

Software Application:

Total Number of Sequences: 17

Total Nucleotides: 0

Total Amino Acids: 0

Number of Errors: 38

Number of Warnings: 32

Number of Corrections: 0

MESSAGE SUMMARY

200 E: 2 (Mandatory Header Field missing)

201 W: 17 (Mandatory field data missing)

203 E: 1 (No. of Seq. differs)

210 E: 17 ((40) Invalid Number of Sequences)

212 E: 1 ((34) Invalid or duplicate Sequence ID Number)

259 W: 14 (Allowed number of lines exceeded)

282 W: 1 (Numeric Field Identifier Missing)

310 E: 17 ((3) Wrong or Missing Sequence Type)